

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: BENOIT, Patrick  
MEYER, Francois  
MAGUIRE, Deborah  
PLAVEC, Ivan  
TOVEY, Michael G.

(ii) TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I INTERFERON

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Foley & Lardner  
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(C) CITY: Washington  
(D) STATE: D.C.  
(E) ZIP: 20007

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/307,588  
(B) FILING DATE: 05-DEC-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/EP93/00770  
(B) FILING DATE: 30-MAR-1993

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: EP 92400902.0  
(B) FILING DATE: 31-MAR-1992

(ix) ATTORNEY/AGENT INFORMATION:

(A) NAME: SAXE, Bernhard D.  
(B) REGISTRATION NUMBER: 28,665  
(C) REFERENCE/DOCKET NUMBER: 17283/117/GUPL

(x) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (202) 672-5300  
(B) TELEFAX: (202) 672-5399

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1343 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 27..1334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTGCAGGGAT CTGCGGCGGC TCCCCAG ATG ATG GTC GTC CTC CTG GGC GCG ACG 53  
Met Met Val Val Leu Leu Gly Ala Thr  
1 5

ACC CTA GTG CTC GTC GCC GTG GGC CCA TGG GTG TTG TCC GCA GCC GCA 101  
Thr Leu Val Leu Val Ala Val Gly Pro Trp Val Leu Ser Ala Ala Ala  
10 15 20 25

GGT GGA AAA AAT CTA AAA TCT CCT CAA AAA GTC GAG GTC GAC ATC ATA 149  
Gly Gly Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile Ile  
30 35 40

GAT GAC AAC TTT ATC CTG AGG TGG AAC AGG AGC GAT GAG TCT GTC GGG 197  
Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val Gly  
45 50 55

AAT GTG ACT TTT TCA TTC GAT TAT CAA AAA ACT GGG ATG GAT AAT TGG 245  
Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp  
60 65 70

ATA AAA TTG TCT GGG TGT CAG AAT ATT ACT AGT ACC AAA TGC AAC TTT 293  
Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn Phe  
75 80 85

TCT TCA CTC AAG CTG AAT GTT TAT GAA GAA ATT AAA TTG CGT ATA AGA 341  
Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg  
90 95 100 105

GCA GAA AAA GAA AAC ACT TCT TCA TGG TAT GAG GTT GAC TCA TTT ACA 389  
Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr  
110 115 120

CCA TTT CGC AAA GCT CAG ATT GGT CCT CCA GAA GTA CAT TTA GAA GCT 437  
Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala  
125 130 135

GAA GAT AAG GCA ATA GTG ATA CAC ATC TCT CCT GGA ACA AAA GAT AGT 485  
Glu Asp Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser  
140 145 150

GTT ATG TGG GCT TTG GAT GGT TTA AGC TTT ACA TAT AGC TTA CTT ATC 533  
Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Leu Ile  
155 160 165

TGG AAA AAC TCT TCA GGT GTA GAA GAA AGG ATT GAA AAT ATT TAT TCC 581  
Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser  
170 175 180 185

AGA CAT AAA ATT TAT AAA CTC TCA CCA GAG ACT ACT TAT TGT CTA AAA 629  
Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys  
190 195 200

GTT AAA GCA GCA CTA CTT ACG TCA TGG AAA ATT GGT GTC TAT AGT CCA 677  
Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro  
205 210 215

GTA CAT TGT ATA AAG ACC ACA GTT GAA AAT GAA CTA CCT CCA CCA GAA 725  
Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu  
220 225 230 235

AAT ATA GAA GTC AGT GTC CAA AAT CAG AAC TAT GTT CTT AAA TGG GAT 773  
Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp  
235 240 245

TAT ACA TAT GCA AAC ATG ACC TTT CAA GTT CAG TGG CTC CAC GCC TTT 821  
Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe  
250 255 260 265

TTA AAA AGG AAT CCT GGA AAC CAT TTG TAT AAA TGG AAA CAA ATA CCT 869  
Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro  
270 275 280

GAC TGT GAA AAT GTC AAA ACT ACC CAG TGT GTC TTT CCT CAA AAC GTT 917  
Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val  
285 290 295

TTC CAA AAA GGA ATT TAC CTT CTC CGC GTA CAA GCA TCT GAT GGA AAT 965  
Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp Gly Asn  
300 305 310

AAC ACA TCT TTT TGG TCT GAA GAG ATA AAG TTT GAT ACT GAA ATA CAA 1013  
Asn Thr Ser Phe Trp Ser Glu Ile Lys Phe Asp Thr Glu Ile Gln  
315 320 325

GCT TTC CTA CTT CCT CCA GTC TTT AAC ATT AGA TCC CTT AGT GAT TCA 1061  
Ala Phe Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser  
330 335 340 345

TTC CAT ATC TAT ATC GGT GCT CCA AAA CAG TCT GGA AAC ACG CCT GTG 1109  
Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val  
350 355 360

ATC CAG GAT TAT CCA CTG ATT TAT GAA ATT ATT TTT TGG GAA AAC ACT 1157  
Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr  
365 370 375

TCA AAT GCT GAG AGA AAA ATT ATC GAG AAA AAA ACT GAT GTT ACA GTT 1205  
Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val  
380 385 390

CCT AAT TTG AAA CCA CTG ACT GTA TAT TGT GTG AAA GCC AGA GCA CAC 1253  
Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His  
395 400 405

ACC ATG GAT GAA AAG CTG AAT AAA AGC AGT GTT TTT AGT GAC GCT GTA 1301  
Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val  
410 415 420 425

TGT GAG AAA ACA AAA CCA GGA AAT ACC TCT AAA TGAGGTACC 1343  
Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys  
430 435

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 436 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Met Val Val Leu Leu Gly Ala Thr Thr Leu Val Leu Val Ala Val  
1 5 10 15  
Gly Pro Trp Val Leu Ser Ala Ala Gly Gly Lys Asn Leu Lys Ser  
20 25 30

Pro Gln Lys Val Glu Val Asp Ile Ile Asp Asp Asn Phe Ile Leu Arg  
35 40 45

Trp Asn Arg Ser Asp Glu Ser Val Gly Asn Val Thr Phe Ser Phe Asp  
50 55 60

Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys Leu Ser Gly Cys Gln  
65 70 75 80

Asn Ile Thr Ser Thr Lys Cys Asn Phe Ser Ser Leu Lys Leu Asn Val  
85 90 95

Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu Lys Glu Asn Thr Ser  
100 105 110

Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe Arg Lys Ala Gln Ile  
115 120 125

Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp Lys Ala Ile Val Ile  
130 135 140

His Ile Ser Pro Gly Thr Lys Asp Ser Val Met Trp Ala Leu Asp Gly  
145 150 155 160

Leu Ser Phe Thr Tyr Ser Leu Leu Ile Trp Lys Asn Ser Ser Gly Val  
165 170 175

Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His Lys Ile Tyr Lys Leu  
180 185 190

Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys Ala Ala Leu Leu Thr  
195 200 205

Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His Cys Ile Lys Thr Thr  
210 215 220

Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile Glu Val Ser Val Gln  
225 230 235 240

Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr Tyr Ala Asn Met Thr  
245 250 255

Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys Arg Asn Pro Gly Asn  
260 265 270

His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys Glu Asn Val Lys Thr  
275 280 285

Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln Lys Gly Ile Tyr Leu  
290 295 300

Leu Arg Val Gln Ala Ser Asp Gly Asn Asn Thr Ser Phe Trp Ser Glu  
305 310 315 320

Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe Leu Leu Pro Pro Val  
325 330 335

Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His Ile Tyr Ile Gly Ala  
340 345 350

Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln Asp Tyr Pro Leu Ile  
355 360 365

Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn Ala Glu Arg Lys Ile  
370 375 380

Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn Leu Lys Pro Leu Thr  
385 390 395 400  
Val Tyr Cys Val Lys Ala Arg Ala His Thr Met Asp Glu Lys Leu Asn  
405 410 415  
Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu Lys Thr Lys Pro Gly  
420 425 430  
Asn Thr Ser Lys  
435

*S261C7*  
(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1755 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 27..1697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTGCAGGGAT CTGCGGCCGGC TCCCCAG ATG ATG GTC GTC CTC CTG GGC GCG ACG 53  
Met Met Val Val Leu Leu Gly Ala Thr  
1 5  
ACC CTA GTG CTC GTC GCC GTG GGC CCA TGG GTG TTG TCC GCA GCC GCA 101  
Thr Leu Val Leu Val Ala Val Gly Pro Trp Val Leu Ser Ala Ala Ala  
10 15 20 25  
GGT GGA AAA AAT CTA AAA TCT CCT CAA AAA GTA GAG GTC GAC ATC ATA 149  
Gly Gly Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile Ile  
30 35 40  
GAT GAC AAC TTT ATC CTG AGG TGG AAC AGG AGC GAT GAG TCT GTC GGG 197  
Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val Gly  
45 50 55  
AAT GTG ACT TTT TCA TTC GAT TAT CAA AAA ACT GGG ATG GAT AAT TGG 245  
Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp  
60 65 70  
ATA AAA TTG TCT GGG TGT CAG AAT ATT ACT AGT ACC AAA TGC AAC TTT 293  
Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn Phe  
75 80 85  
TCT TCA CTC AAG CTG AAT GTT TAT GAA GAA ATT AAA TTG CGT ATA AGA 341  
Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg  
90 95 100 105  
GCA GAA AAA GAA AAC ACT TCT TCA TGG TAT GAG GTT GAC TCA TTT ACA 389  
Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr  
110 115 120  
CCA TTT CGC AAA GCT CAG ATT GGT CCT CCA GAA GTA CAT TTA GAA GCT 437  
Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala  
125 130 135

GAA	GAT	AAG	GCA	ATA	GTG	ATA	CAC	ATC	TCT	CCT	GGA	ACA	AAA	GAT	AGT	485
Glu	Asp	Lys	Ala	Ile	Val	Ile	His	Ile	Ser	Pro	Gly	Thr	Lys	Asp	Ser	
140						145						150				
GTT	ATG	TGG	GCT	TTG	GAT	GGT	TTA	AGC	TTT	ACA	TAT	AGC	TTA	CTT	ATC	533
Val	Met	Trp	Ala	Leu	Asp	Gly	Leu	Ser	Phe	Thr	Tyr	Ser	Leu	Leu	Ile	
155						160					165					
TGG	AAA	AAC	TCT	TCA	GGT	GTA	GAA	GAA	AGG	ATT	GAA	AAT	ATT	TAT	TCC	581
Trp	Lys	Asn	Ser	Ser	Gly	Val	Glu	Glu	Arg	Ile	Glu	Asn	Ile	Tyr	Ser	
170						175					180				185	
AGA	CAT	AAA	ATT	TAT	AAA	CTC	TCA	CCA	GAG	ACT	ACT	TAT	TGT	CTA	AAA	629
Arg	His	Lys	Ile	Tyr	Lys	Leu	Ser	Pro	Glu	Thr	Thr	Tyr	Tyr	Cys	Leu	Lys
190							195								200	
GTT	AAA	GCA	GCA	CTA	CTT	ACG	TCA	TGG	AAA	ATT	GGT	GTC	TAT	AGT	CCA	677
Val	Lys	Ala	Ala	Leu	Leu	Thr	Ser	Trp	Lys	Ile	Gly	Val	Tyr	Ser	Pro	
205							210						215			
GTA	CAT	TGT	ATA	AAG	ACC	ACA	GTT	GAA	AAT	GAA	CTA	CCT	CCA	CCA	GAA	725
Val	His	Cys	Ile	Lys	Thr	Thr	Val	Glu	Asn	Glu	Leu	Pro	Pro	Pro	Pro	
220							225								230	
AAT	ATA	GAA	GTC	AGT	GTC	CAA	AAT	CAG	AAC	TAT	GTT	CTT	AAA	TGG	GAT	773
Asn	Ile	Glu	Val	Ser	Val	Gln	Asn	Gln	Asn	Tyr	Val	Leu	Lys	Trp	Asp	
235						240					245					
TAT	ACA	TAT	GCA	AAC	ATG	ACC	TTT	CAA	GTT	CAG	TGG	CTC	CAC	GCC	TTT	821
Tyr	Thr	Tyr	Ala	Asn	Met	Thr	Phe	Gln	Val	Gln	Trp	Leu	His	Ala	Phe	
250						255					260				265	
TTA	AAA	AGG	AAT	CCT	GGA	AAC	CAT	TTG	TAT	AAA	TGG	AAA	CAA	ATA	CCT	869
Leu	Lys	Arg	Asn	Pro	Gly	Asn	His	Leu	Tyr	Lys	Trp	Lys	Gln	Ile	Pro	
270							275								280	
GAC	TGT	GAA	AAT	GTC	AAA	ACT	ACC	CAG	TGT	GTC	TTT	CCT	CAA	AAC	GTT	917
Asp	Cys	Glu	Asn	Val	Lys	Thr	Thr	Gln	Cys	Val	Phe	Pro	Gln	Asn	Val	
285							290								295	
TTC	CAA	AAA	GGA	ATT	TAC	CTT	CTC	CGC	GTA	CAA	GCA	TCT	GAT	GGA	AAT	965
Phe	Gln	Lys	Gly	Ile	Tyr	Leu	Leu	Arg	Val	Gln	Ala	Ser	Asp	Gly	Asn	
300						305						310				
AAC	ACA	TCT	TTT	TGG	TCT	GAA	GAG	ATA	AAG	TTT	GAT	ACT	GAA	ATA	CAA	1013
Asn	Thr	Ser	Phe	Trp	Ser	Glu	Glu	Ile	Lys	Phe	Asp	Thr	Glu	Ile	Gln	
315						320					325					
GCT	TTC	CTA	CTT	CCT	CCA	GTC	TTT	AAC	ATT	AGA	TCC	CTT	AGT	GAT	TCA	1061
Ala	Phe	Leu	Leu	Pro	Pro	Val	Phe	Asn	Ile	Arg	Ser	Leu	Ser	Asp	Ser	
330						335					340				345	
TTC	CAT	ATC	TAT	ATC	GGT	GCT	CCA	AAA	CAG	TCT	GGA	AAC	ACG	CCT	GTG	1109
Phe	His	Ile	Tyr	Ile	Gly	Ala	Pro	Lys	Gln	Ser	Gly	Asn	Thr	Pro	Val	
350						355									360	
ATC	CAG	GAT	TAT	CCA	CTG	ATT	TAT	GAA	ATT	ATT	TCT	TGG	GAA	AAC	ACT	1157
Ile	Gln	Asp	Tyr	Pro	Leu	Ile	Tyr	Glu	Ile	Ile	Phe	Trp	Glu	Asn	Thr	
365						370						375				
TCA	AAT	GCT	GAG	AGA	AAA	ATT	ATC	GAG	AAA	AAA	ACT	GAT	GTT	ACA	GTT	1205
Ser	Asn	Ala	Glu	Arg	Lys	Ile	Ile	Glu	Lys	Lys	Thr	Asp	Val	Thr	Val	
380						385						390				
CCT	AAT	TTG	AAA	CCA	CTG	ACT	GTA	TAT	TGT	GTG	AAA	GCC	AGA	GCA	CAC	1253
Pro	Asn	Leu	Lys	Pro	Leu	Thr	Val	Tyr	Cys	Val	Lys	Ala	Arg	Ala	His	
395						400						405				

ACC ATG GAT GAA AAG CTG AAT AAA AGC AGT GTT TTT AGT GAC GCT GTA 1301  
Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val  
410 415 420 425

TGT GAG AAA ACA AAA CCA GGA AAT ACC TCT AAA ATT TGG CTT ATA GTT 1349  
Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys Ile Trp Leu Ile Val  
430 435 440

GGA ATT TGT ATT GCA TTA TTT GCT CTC CCG TTT GTC ATT TAT GCT GCG 1397  
Gly Ile Cys Ile Ala Leu Phe Ala Leu Pro Phe Val Ile Tyr Ala Ala  
445 450 455

AAA GTC TTC TTG AGA TGC ATC AAT TAT GTC TTC TTT CCA TCA CTT AAA 1445  
Lys Val Phe Leu Arg Cys Ile Asn Tyr Val Phe Phe Pro Ser Leu Lys  
460 465 470

*S241*

CCT TCT TCC AGT ATA GAT GAG TAT TTC TCT GAA CAG CCA TTG AAG AAT 1493  
Pro Ser Ser Ile Asp Glu Tyr Phe Ser Glu Gln Pro Leu Lys Asn  
475 480 485

CTT CTG CTT TCA ACT TCT GAG GAA CAA ATC GAA AAA TGT TTC ATA ATT 1541  
Leu Leu Leu Ser Thr Ser Glu Glu Gln Ile Glu Lys Cys Phe Ile Ile  
490 495 500 505

GAA AAT ATA AGC ACA ATT GCT ACA GTA GAA GAA ACT AAT CAA ACT GAT 1589  
Glu Asn Ile Ser Thr Ile Ala Thr Val Glu Glu Thr Asn Gln Thr Asp  
510 515 520

GAA GAT CAT AAA AAA TAC AGT TCC CAA ACT AGC CAA GAT TCA GGA AAT 1637  
Glu Asp His Lys Lys Tyr Ser Ser Gln Thr Ser Gln Asp Ser Gly Asn  
525 530 535

TAT TCT AAT GAA GAT GAA AGC GAA AGT AAA ACA AGT GAA GAA CTA CAG 1685  
Tyr Ser Asn Glu Asp Glu Ser Glu Ser Lys Thr Ser Glu Glu Leu Gln  
540 545 550

CAG GAC TTT GTA TGACCAAGAAA TGAACGTGTGT CAAGTATAAG GTTTTCAGC 1737  
Gln Asp Phe Val  
555

AGGAGTTACA CTGGTACC 1755

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 557 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Met Val Val Leu Leu Gly Ala Thr Thr Leu Val Leu Val Ala Val  
1 5 10 15

Gly Pro Trp Val Leu Ser Ala Ala Gly Gly Lys Asn Leu Lys Ser  
20 25 30

Pro Gln Lys Val Glu Val Asp Ile Ile Asp Asp Asn Phe Ile Leu Arg  
35 40 45

Trp Asn Arg Ser Asp Glu Ser Val Gly Asn Val Thr Phe Ser Phe Asp  
50 55 60

Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys Leu Ser Gly Cys Gln  
65 70 75 80

Asn Ile Thr Ser Thr Lys Cys Asn Phe Ser Ser Leu Lys Leu Asn Val  
85 90 95

Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu Lys Glu Asn Thr Ser  
100 105 110

Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe Arg Lys Ala Gln Ile  
115 120 125

Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp Lys Ala Ile Val Ile  
130 135 140

His Ile Ser Pro Gly Thr Lys Asp Ser Val Met Trp Ala Leu Asp Gly  
145 150 155 160

Leu Ser Phe Thr Tyr Ser Leu Leu Ile Trp Lys Asn Ser Ser Gly Val  
165 170 175

Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His Lys Ile Tyr Lys Leu  
180 185 190

Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys Ala Ala Leu Leu Thr  
195 200 205

Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His Cys Ile Lys Thr Thr  
210 215 220

Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile Glu Val Ser Val Gln  
225 230 235 240

Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr Tyr Ala Asn Met Thr  
245 250 255

Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys Arg Asn Pro Gly Asn  
260 265 270

His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys Glu Asn Val Lys Thr  
275 280 285

Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln Lys Gly Ile Tyr Leu  
290 295 300

Leu Arg Val Gln Ala Ser Asp Gly Asn Asn Thr Ser Phe Trp Ser Glu  
305 310 315 320

Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe Leu Leu Pro Pro Val  
325 330 335

Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His Ile Tyr Ile Gly Ala  
340 345 350

Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln Asp Tyr Pro Leu Ile  
355 360 365

Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn Ala Glu Arg Lys Ile  
370 375 380

Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn Leu Lys Pro Leu Thr  
385 390 395 400

Val Tyr Cys Val Lys Ala Arg Ala His Thr Met Asp Glu Lys Leu Asn  
405 410 415

Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu Lys Thr Lys Pro Gly  
420 425 430

Asn Thr Ser Lys Ile Trp Leu Ile Val Gly Ile Cys Ile Ala Leu Phe  
435 440 445

Ala Leu Pro Phe Val Ile Tyr Ala Ala Lys Val Phe Leu Arg Cys Ile  
450 455 460

Asn Tyr Val Phe Phe Pro Ser Leu Lys Pro Ser Ser Ser Ile Asp Glu  
465 470 475 480

Tyr Phe Ser Glu Gln Pro Leu Lys Asn Leu Leu Leu Ser Thr Ser Glu  
485 490 495

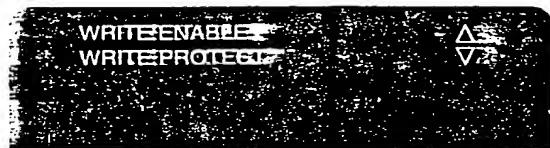
Glu Gln Ile Glu Lys Cys Phe Ile Ile Glu Asn Ile Ser Thr Ile Ala  
500 505 510

Thr Val Glu Glu Thr Asn Gln Thr Asp Glu Asp His Lys Lys Tyr Ser  
515 520 525

Ser Gln Thr Ser Gln Asp Ser Gly Asn Tyr Ser Asn Glu Asp Glu Ser  
530 535 540

Glu Ser Lys Thr Ser Glu Glu Leu Gln Gln Asp Phe Val  
545 550 555

0 6 2 0 2 0 - 5 2 0 2 0 6 0



IBM PC AT 1.44mb MSDOS 3.3  
BENOIT, et al.  
US 08/307,588  
FILED: 05-DEC-1994  
"MONOCLONAL ANTIBODIES  
AGAINST THE INTERFERON..."  
ATTY DOCKET: 17283/117/GUPL  
DATA REC'D: 26 MAR 1996